

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,711

DATE: 08/30/2001

TIME: 07:37:03

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\08302001\I701711.raw

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6 <120> TITLE OF INVENTION: Novel Compounds
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12 <140> CURRENT APPLICATION NUMBER: US 09/701,711
13 <141> CURRENT FILING DATE: 2000-12-01
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16 <151> PRIOR FILING DATE: 1999-05-31
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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24 <212> TYPE: DNA
25 <213> ORGANISM: Moraxella catarrhalis
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30 ctacagcgag tgaccattga aagcttacaa agcgtgctgc cgtttcgctt ggggtcaagtg      180
31 gtgagcgaaa accagttggc tgatggtgtc aaagcacttt atgcaacagg caatttttca      240
32 gatgtgcaag tctatcatca agaaggcggt atcatctatc aggtaaccga aaggccgtta      300
33 atcgttgaga ttaattttga gggcaatcgc ttaattccaa aagaaggctc acaagaaggg      360
34 ctaaaaaatg ctggccttagc tgtgggtcaa ccactaaaac aagccacagt acagatgatc      420
35 gaaaccgagc ttaccaatca atatatatca caaggctatt ataataccga aattactgtc      480
36 aaacagacga tgcttgatgg taatcgtggt aagcttgata tgacctttgc tgaaggtaaa      540
37 cctgcacggg tggttgatat taatatcatt ggcaatcagc attttagcga tgcagatttg      600
38 attgatgtgc ttgcgattaa ggataataaa atcaatccac tgtctaaagc tgaccgttat      660
39 actcaagaaa agctggtgac cagtttagag aatttgctg ctaaatatct caatgcaggg      720
40 tttgtgctgt ttgagattaa agatgctaag cttaatatca atgaagataa aaaccgtatc      780
41 tttgttgaga ttctattgca tgaagggtgag caatatcgtt ttggacagac acagtttttg      840
42 ggtaatttaa cttatactca agcagaactt gaggcactgc ttaaattcaa agcagaagaa      900
43 gggttttcac aagccatgct tgagcaaaca acaaacataa tcagtaccaa atttggtgac      960
44 gatggctatt attatgctca aatccgtcct gtaacacgca ttaatgatga aagtcgtacg      1020
45 gttgatgtgg aatattatat tgaccctgta caccctgtct atgtacgccg tattaatttt      1080
46 acaggtaact ttaagacca agatgaagta ctccgtcgtg agatgcgaca acttgaagggt      1140
47 gcgttggcat ctaatcaaaa aatccagctg tctcgtgcac gcttgatgcg gactgggttt      1200
48 tttaaactatg ttaccgttga tactcgtcca gtacccaact cacctgatca ggttgatgta      1260
49 aattttgtgg ttgaagaaca accttcagga tcatcaacca tcgcagcagg ctactctcaa      1320
50 agtgggtggg taacttttca atttgatggt tctcaaaata actttatggg tacaggtaag      1380
51 caggtcaatg cttcgttttc tcgctctgag acccgtgagg tgtatagttt gggatgacc      1440
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53 aagtatgata acaagaacat tagtaattat gtaacttgat cttatggtgg ctcattaagc      1560
54 tatgatatc caattgatga aaatcaacgc ataagctttg gtctgaatgc tgacaatacc      1620
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56 ggcaaaattc aagtggataa taatggcatt cctgatttta agcatgatta cacaacctac      1740
57 aatgccattt tgggggtgaa ttattcaagt ctagatcgcc ctgtatttcc aaccaaggc      1800
58 atgagtcatt ctgtagattt gacggttggt tttggtgata aaactcatca aaaagtgggt      1860
59 tatcaaggca atatctatcg cccattttat aaaaaatcag tcttgctggg atacgccaag      1920
60 ttaggctatg gcaataattt accattttat gaaaatttct atgcaggcgg ctatggttcg      1980

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61 gttcgtggct atgatcaatc ctctttgggt ccacgtcac aagcctatatt gacagctcgt      2040
62 cgtgggtcaac aaaccacact aggagaggtt gttgggtgga atgctttggc aactttcggc      2100
63 agtgagctga ttttaccttt gccatttaaa ggtgattgga tagatcaggt gcgtccagtg      2160
64 atattcattg agggcggtca ggtttttgat acaacaggta tggataaaca aaccattgat      2220
65 ttaacccaat ttaaagacct acaagcaaca gctgaacaaa atgcaaaaagc agccaatcgc      2280
66 ccgctactaa cccaagataa acagttgcgt tatagtgctg gtggttggtgc aacttggtat      2340
67 acgcccattg gtcctttatc tattagctat gccaagccat tgaataaaaa acaaaatgat      2400
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72 <212> TYPE: PRT
73 <213> ORGANISM: Moraxella catarrhalis
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80 Ala Asn Asp Ile Thr Ile Thr Gly Leu Gln Arg Val Thr Ile Glu Ser
81 35 40 45
82 Leu Gln Ser Val Leu Pro Phe Arg Leu Gly Gln Val Val Ser Glu Asn
83 50 55 60
84 Gln Leu Ala Asp Gly Val Lys Ala Leu Tyr Ala Thr Gly Asn Phe Ser
85 65 70 75 80
86 Asp Val Gln Val Tyr His Gln Glu Gly Arg Ile Ile Tyr Gln Val Thr
87 85 90 95
88 Glu Arg Pro Leu Ile Ala Glu Ile Asn Phe Glu Gly Asn Arg Leu Ile
89 100 105 110
90 Pro Lys Glu Gly Leu Gln Glu Gly Leu Lys Asn Ala Gly Leu Ala Val
91 115 120 125
92 Gly Gln Pro Leu Lys Gln Ala Thr Val Gln Met Ile Glu Thr Glu Leu
93 130 135 140
94 Thr Asn Gln Tyr Ile Ser Gln Gly Tyr Tyr Asn Thr Glu Ile Thr Val
95 145 150 155 160
96 Lys Gln Thr Met Leu Asp Gly Asn Arg Val Lys Leu Asp Met Thr Phe
97 165 170 175
98 Ala Glu Gly Lys Pro Ala Arg Val Val Asp Ile Asn Ile Ile Gly Asn
99 180 185 190
100 Gln His Phe Ser Asp Ala Asp Leu Ile Asp Val Leu Ala Ile Lys Asp
101 195 200 205
102 Asn Lys Ile Asn Pro Leu Ser Lys Ala Asp Arg Tyr Thr Gln Glu Lys
103 210 215 220
104 Leu Val Thr Ser Leu Glu Asn Leu Arg Ala Lys Tyr Leu Asn Ala Gly
105 225 230 235 240
106 Phe Val Arg Phe Glu Ile Lys Asp Ala Lys Leu Asn Ile Asn Glu Asp
107 245 250 255
108 Lys Asn Arg Ile Phe Val Glu Ile Ser Leu His Glu Gly Glu Gln Tyr
109 260 265 270
110 Arg Phe Gly Gln Thr Gln Phe Leu Gly Asn Leu Thr Tyr Thr Gln Ala
111 275 280 285

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112 Glu Leu Glu Ala Leu Leu Lys Phe Lys Ala Glu Glu Gly Phe Ser Gln
113      290      295      300
114 Ala Met Leu Glu Gln Thr Thr Asn Asn Ile Ser Thr Lys Phe Gly Asp
115 305      310      315      320
116 Asp Gly Tyr Tyr Tyr Ala Gln Ile Arg Pro Val Thr Arg Ile Asn Asp
117      325      330      335
118 Glu Ser Arg Thr Val Asp Val Glu Tyr Tyr Ile Asp Pro Val His Pro
119      340      345      350
120 Val Tyr Val Arg Arg Ile Asn Phe Thr Gly Asn Phe Lys Thr Gln Asp
121      355      360      365
122 Glu Val Leu Arg Arg Glu Met Arg Gln Leu Glu Gly Ala Leu Ala Ser
123      370      375      380
124 Asn Gln Lys Ile Gln Leu Ser Arg Ala Arg Leu Met Arg Thr Gly Phe
125 385      390      395      400
126 Phe Lys His Val Thr Val Asp Thr Arg Pro Val Pro Asn Ser Pro Asp
127      405      410      415
128 Gln Val Asp Val Asn Phe Val Val Glu Glu Gln Pro Ser Gly Ser Ser
129      420      425      430
130 Thr Ile Ala Ala Gly Tyr Ser Gln Ser Gly Gly Val Thr Phe Gln Phe
131      435      440      445
132 Asp Val Ser Gln Asn Asn Phe Met Gly Thr Gly Lys His Val Asn Ala
133      450      455      460
134 Ser Phe Ser Arg Ser Glu Thr Arg Glu Val Tyr Ser Leu Gly Met Thr
135 465      470      475      480
136 Asn Pro Tyr Phe Thr Val Asn Gly Val Ser Gln Ser Leu Ser Gly Tyr
137      485      490      495
138 Tyr Arg Lys Thr Lys Tyr Asp Asn Lys Asn Ile Ser Asn Tyr Val Leu
139      500      505      510
140 Asp Ser Tyr Gly Gly Ser Leu Ser Tyr Gly Tyr Pro Ile Asp Glu Asn
141      515      520      525
142 Gln Arg Ile Ser Phe Gly Leu Asn Ala Asp Asn Thr Lys Leu His Gly
143      530      535      540
144 Gly Arg Phe Met Gly Ile Ser Asn Val Lys Gln Leu Met Ala Asp Gly
145 545      550      555      560
146 Gly Lys Ile Gln Val Asp Asn Asn Gly Ile Pro Asp Phe Lys His Asp
147      565      570      575
148 Tyr Thr Thr Tyr Asn Ala Ile Leu Gly Trp Asn Tyr Ser Ser Leu Asp
149      580      585      590
150 Arg Pro Val Phe Pro Thr Gln Gly Met Ser His Ser Val Asp Leu Thr
151      595      600      605
152 Val Gly Phe Gly Asp Lys Thr His Gln Lys Val Val Tyr Gln Gly Asn
153      610      615      620
154 Ile Tyr Arg Pro Phe Ile Lys Lys Ser Val Leu Arg Gly Tyr Ala Lys
155 625      630      635      640
156 Leu Gly Tyr Gly Asn Asn Leu Pro Phe Tyr Glu Asn Phe Tyr Ala Gly
157      645      650      655
158 Gly Tyr Gly Ser Val Arg Gly Tyr Asp Gln Ser Ser Leu Gly Pro Arg
159      660      665      670
160 Ser Gln Ala Tyr Leu Thr Ala Arg Arg Gly Gln Gln Thr Thr Leu Gly

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161		675		680		685	
162	Glu	Val	Val	Gly	Gly	Asn	Ala
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164	Leu	Pro	Leu	Pro	Phe	Lys	Gly
165	705			710		715	
166	Ile	Phe	Ile	Glu	Gly	Gly	Gln
167				725		730	
168	Gln	Thr	Ile	Asp	Leu	Thr	Gln
169				740		745	
170	Gln	Asn	Ala	Lys	Ala	Ala	Asn
171				755		760	
172	Leu	Arg	Tyr	Ser	Ala	Gly	Val
173				770		775	
174	Pro	Leu	Ser	Ile	Ser	Tyr	Ala
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179	<210> SEQ ID NO: 3						
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188	gtgagcgaaa	accagttggc	tgatggtgct	aaagcacttt	atgcaacagg	caatttttca	240
189	gatgtgcaag	tctatcatca	agaagggcgt	atcatctatc	aggtaaccga	aaggccggtta	300
190	atcgctgaga	ttatttttga	gggcaatcgc	ttatttccaa	aagaaggctt	acaagaaggg	360
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192	gaaaccgagc	ttaccaatca	atatatatca	caaggctatt	ataataccga	aattactgtc	480
193	aaacagacga	tgcttgatgg	taatcgtggt	aagcttgata	tgacctttgc	tgaaggtaaa	540
194	cctgcacggg	tggttgatat	taatatcatt	ggcaatcagc	atttttagcg	tgacagattg	600
195	attgatgtgc	ttgcgattaa	ggataataaa	atcaatccac	tgtctaaagc	tgaccgttat	660
196	actcaagaaa	agctgggtgac	cagtttagag	aatttgcgtg	ctaaatatct	caatgcaggg	720
197	tttgtgcgtt	ttgagattaa	agatgctaag	cttaatatca	atgaagataa	aaaccgtatc	780
198	tttgttgaga	tttcatttga	tgaagggtgag	caatatcgct	ttggacagac	acagtttttg	840
199	ggtaatttaa	cttatactca	agcagaactt	gaggcactgc	ttaaattcaa	agcagaagaa	900
200	gggttttcac	aagccatgct	tgagcaaaaca	acaaacaata	tcagtaccaa	atttggtgac	960
201	gatggctatt	attatgctca	aatccgtcct	gtaacacgca	ttaatgatga	aagtcgtacg	1020
202	gttgatgtgg	aatattatat	tgaccctgta	caccctgtct	atgtacgccg	tattaatttt	1080
203	acaggttaact	ttagacccca	agatgaagta	ctccgtcgctg	agatgcgaca	acttgaaggt	1140
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207	agtgggtgg	taacttttca	atttgatggt	tctcaaaata	actttatggg	tacaggttaag	1380
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209	aaccataact	ttaccgtaaa	tgccgtctcg	caaagcttga	gtggctacta	tcgtaaaacc	1500
210	aagtatgata	acaagaacat	tagtaattat	gtacttgatt	cttatgggtg	ctcattaagc	1560
211	tatggatatc	caattgatga	aatcaacgc	ataagctttg	gtctgaatgc	tgacaatacc	1620

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212 aagcttcattg gcggtcggtt tatgggcatt agtaatgtca agcagctgat ggcagatggt 1680
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214 aatgccattt tggggtggaa ttattcaagt ctagatcgcc ctgtatttcc aacccaaggc 1800
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217 ttaggctatg gcaataattt accattttat gaaaatttct atgcaggcgg ctatggttcg 1980
218 gttcgtggct atgatcaatc ctctttgggt ccacgctcac aagcctattt gacagctcgt 2040
219 cgtggtcaac aaaccacact aggagagggt gttggtggtg atgctttggc aactttcggc 2100
220 agtgagctga ttttaccttt gccatttaaa ggtgattgga tagatcagggt gcgtccagtg 2160
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222 ttaacccaat ttaaagacct acaagcaaca gctgaacaaa atgcaaaagc agccaatcgc 2280
223 ccgctactaa cccaagataa acagttgcgt tatagtgcgt gtgttggtgc aacttggtat 2340
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227 <210> SEQ ID NO: 4
228 <211> LENGTH: 813
229 <212> TYPE: PRT
230 <213> ORGANISM: Moraxella catarrhalis
232 <400> SEQUENCE: 4
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238 35 40 45
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240 50 55 60
241 Gln Leu Ala Asp Gly Val Lys Ala Leu Tyr Ala Thr Gly Asn Phe Ser
242 65 70 75 80
243 Asp Val Gln Val Tyr His Gln Glu Gly Arg Ile Ile Tyr Gln Val Thr
244 85 90 95
245 Glu Arg Pro Leu Ile Ala Glu Ile Asn Phe Glu Gly Asn Arg Leu Ile
246 100 105 110
247 Pro Lys Glu Gly Leu Gln Glu Gly Leu Lys Asn Ala Gly Leu Ala Val
248 115 120 125
249 Gly Gln Pro Leu Lys Gln Ala Thr Val Gln Met Ile Glu Thr Glu Leu
250 130 135 140
251 Thr Asn Gln Tyr Ile Ser Gln Gly Tyr Tyr Asn Thr Glu Ile Thr Val
252 145 150 155 160
253 Lys Gln Thr Met Leu Asp Gly Asn Arg Val Lys Leu Asp Met Thr Phe
254 165 170 175
255 Ala Glu Gly Lys Pro Ala Arg Val Val Asp Ile Asn Ile Ile Gly Asn
256 180 185 190
257 Gln His Phe Ser Asp Ala Asp Leu Ile Asp Val Leu Ala Ile Lys Asp
258 195 200 205
259 Asn Lys Ile Asn Pro Leu Ser Lys Ala Asp Arg Tyr Thr Gln Glu Lys
260 210 215 220
261 Leu Val Thr Ser Leu Glu Asn Leu Arg Ala Lys Tyr Leu Asn Ala Gly
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VERIFICATION SUMMARY

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